

Supplemental Table 1. Sequences for qPCR, shRNA primers and binding sequences of pmirGlo vector.

NSUN2-F	CTGGTTACAAAAGCCACGCA	qPCR primer for human genes
NSUN2-R	CTTTCTGACCGTCCACCTCC	
FSP1-F	CTGAACGTCCCCTTCATGCT	
FSP1-R	GTCTTTTGGCGAACCTGTC	
YBX1-F	TCCCACCTTACTACATGCG	
YBX1-R	CTTGTTCTCCTGCACCCT	
GAPDH-F	GTCTCCTCTGACTTCAACAGCG	
GAPDH-R	ACCACCCTGTTGCTGTAGCCAA	
FSP1_RIPqPCR-F	GGAGAACTACCGCAGCAGGT	
FSP1_RIPqPCR-R	TCAGCTTGCATGCCTGCAGG	
shNSUN2#1-F	CCGGTGCAGTGTCCCATCGTCTTATCTCGAGAT AAGACGATGGGACACTGCATTTTTG	shRNA primers
shNSUN2#1-R	AATTCAAAAATGCAGTGTCCCATCGTCTTATCT CGAGATAAGACGATGGGACACTGCA	
shNSUN2#2-F	CCGGGAGCGATGCCTTAGGATATTACTCGAGT AATATCCTAAGGCATCGCTCTTTTTG	
shNSUN2#2-R	AATTCAAAAAGAGCGATGCCTTAGGATATTAC TCGAGTAATATCCTAAGGCATCGCTC	
shYBX1#1-F	CCGGCCAGTTCAAGGCAGTAAATATCTCGAGA TATTTACTGCCTTGAAGTGGTTTTG	
shYBX1#1-R	AATTCAAAAACCAGTTCAAGGCAGTAAATATC TCGAGATATTTACTGCCTTGAAGTGG	
shYBX1#2-F	CCGGAGCAGACCGTAACCATTATAGCTCGAGC	

	TATAATGGTTACGGTCTGCTTTTTTG	
shYBX1#2-R	AATTCAAAAAAGCAGACCGTAACCATTATAGC TCGAGCTATAATGGTTACGGTCTGCT	
shFSP1#1-F	CCGGATGATGTGGTGGCTAGAAATGCTCGAGC ATTTCTAGCCACCACATCATTTTTTG	
shFSP1#1-R	AATTCAAAAAATGATGTGGTGGCTAGAAATGC TCGAGCATTTCTAGCCACCACATCAT	
shFSP1#2-F	CCGGCCTGCCCTTCTCTCATCTTATCTCGAGAT AAGATGAGAGAAGGGCAGGTTTTTG	
shFSP1#2-R	AATTCAAAAACCTGCCCTTCTCTCATCTTATCT CGAGATAAGATGAGAGAAGGGCAGG	
FSP1-3'UTR-WT-F	AGAGGCCAGGCGGGAGAACTACCGCAGCAGG TGGGCGTACGGACTGCTTGGCGCATGGCACCC GCCTGGCAAGTG	Target sequences for pmirGlo vector
FSP1-3'UTR-WT-R	CACTTGCCAGGCGGGTGCCATGCGCCAAGCAG TCCGTACGCCCACCTGCTGCGGTAGTTC TCCCGCCTGGCCTCT	
FSP1-3'UTR-MUT-F	AGAGGTTAGGTGGGAGAACTACCGCAGCAGGT GGGCGTACGGACTGCTTGGCGCATGGCATTG TCTGGTAAGTG	
FSP1-3'UTR-MUT-R	CACTTACCAGACAAATGCCATGCGCCAAGCAG TCCGTACGCCCACCTGCTGCGGTAGTTC TCCACCTAACCTCT	

Supplementary Table 2. The baseline characteristics of AML patients with low and high NSUN2.

Variables	Low expression	High expression	<i>P</i> value
Number, (%)	151 (49.84)	152 (50.17)	
NSUN2 expression	0.015 [0.011,0.020]	0.142 [0.041, 0.368]	<0.0001
Age, median(range), years	55.00 [38.25, 64.00]	52.00 [38.00,63.00]	0.7145
Male, n (%)	88 (58.28)	81 (53.29)	0.4511
^a WBC, median (^b IQR),X10 ⁹ /L	11.05 [2.40, 49.50]	13.00 [3.20, 67.70]	0.5806
^c HB, median (IQR),X10 ⁹ /L	87.00 (69.00,105.00)	84.00 [66.00, 102.00]	0.3720
^d PLT, median (IQR),X10 ⁹ /L	46.50 [25.25, 86.00]	50.00 [26.00, 90.50]	0.3113
Blast, median (IQR),X10 ⁹ /L	64.25 [39.13, 80.00]	73.00 [49.00,83.88]	0.0633
^e FAB classification, n (%)			0.2934
M0	12 (7.95)	20 (13.16)	
M1	14 (9.27)	13 (8.55)	
M2	81 (53.64)	71 (46.71)	
M3	0	0	
M4	10 (6.62)	4 (2.63)	
M5	29 (19.21)	42 (27.63)	
M6	5 (3.31)	2 (1.32)	
Genes mutations,n(%)			
<i>FLT3-ITD</i>	28 (18.54)	36 (23.68)	0.6936
<i>NPM1</i>	35 (23.18)	40 (26.32)	0.3136

<i>DNMT3a</i>	17 (11.26)	23 (15.13)	0.6940
<i>CEBPA</i> ^{DM, f}	14 (9.27)	22 (14.47)	0.4400
^g Treatment (%)			0.8657
DA	30	34	
HAA	28	23	
IA	85	103	
CR (%)	81 (53.64)	75 (49.34)	0.5097

^aWBC: White blood cell

^bIQR: Interquartile

^cHB: Hemoglobin

^dPLT: Platelet counts

^eFAB: French-American-British classification system

^fDM: Double-allele mutation

^gTreatment: DA = Daunorubicin + Cytarabine, IA = Idarubicin + Cytarabine; HAA:

Homoharringtonine + Cytarabine + Aclarubicin